SEQUENCE LISTING

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      Lofton-Day, Catherine E.
      Yao, Yue

<120> UMLR POLYPEPTIDES

<130> 99-75

<140> 09/695,369
<141> 2000-10-23

<150> 60/160, 880
<151> 1999-10-22

<150> 60/163, 215
<151> 1999-11-02

<150> 60/218,769
<151> 2000-07-17

<150> 60/222,221
<151> 2000-08-01

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                                                   Met Asp Cys Gln
                                                     1

gaa aat gag tac tgg gac caa tgg gga cgg tgt gtc acc tgc caa cgg        163
Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val Thr Cys Gln Arg
 5               10              15                      20

tgt ggt cct gga cag gag cta tcc aag gat tgt ggt tat gga gag ggt        211
Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly Tyr Gly Glu Gly
                 25              30                      35

gga gat gcc tac tgc aca gcc tgc cct cct cgc agg tac aaa agc agc        259
Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg Tyr Lys Ser Ser
             40              45                      50

tgg ggc cac cac aaa tgt cag agt tgc atc acc tgt gct gtc atc aat        307
Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys Ala Val Ile Asn
         55              60                      65

cgt gtt cag aag gtc aac tgc aca gct acc tct aat gct gtc tgt ggg        355
Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn Ala Val Cys Gly
     70              75                      80

gac tgt ttg ccc agg ttc tac cga aag aca cgc att gga ggc ctg cag        403
Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile Gly Gly Leu Gln
 85              90                      95              100

gac caa gag tgc atc ccg tgc acg aag cag acc ccc acc tct gag gtt        451
Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro Thr Ser Glu Val
             105             110                     115

caa tgt gcc ttc cag ttg agc tta gtg gag gca gat gca ccc aca gtg        499
Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala Pro Thr Val
             120             125                     130

ccc cct cag gag gcc aca ctt gtt gca ctg gtg agc agc ctg cta gtg       547
Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser Leu Leu Val
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gtg ttt acc ctg gcc ttc ctg ggg ctc ttc ttc ctc tac tgc aag cag        595
Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr Cys Lys Gln
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ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct        643
Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
165                 170                 175                 180


gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag        691
Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
                185                 190                 195


gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc        739
Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
            200                 205                 210


tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag        787
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
            215                 220                 225


ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag        835
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
    230                 235                 240


acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc        883
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
245                 250                 255                 260


aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaatgag gtctcttggg        933
Asn Val Pro Phe Glu Val Pro Ser Pro  *
                265


cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc     993
aggggcctga aatgtgatgt ccacaagagc taataccota cagatggggc atatcctatc    1053
ccatcccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct    1113
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<213> Homo sapiens

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Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
         35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
     50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
             85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
             100                 105                 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
         115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
     130                 135                 140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145                 150                 155                 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
             165                 170                 175
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
         180                 185                 190
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met
         195                 200                 205
Ala Ser Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile
     210                 215                 220
Glu Cys Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr
225                 230                 235                 240
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             245                 250                 255
Arg Leu Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
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tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn      180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay      240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar      300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty      360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn      420
gcnytngtnw snwsnytnyt ngtngtntty acnytngcnt tyytnggnyt nttyttyytn      480
taytgyaarc arttyttyaa ymgncaytgy carmgnggng gnytnytnca rttygargcn      540
gayaaracng cnaargarga rwsnytntty ccngtnccnc cnwsnaarga racnwsngcn      600
garwsncarg arwsnttyac natggcnwsn tgyacnwsng arwsncayws ncaytgggtn      660
caywsnccna thgartgyac ngarytngay ytncaraart tywsnwsnws ngcnwsntay      720
acnggngcng aracnytngg nggnaayacn gtngarwsna cnggngaymg nytngarytn      780
aaygtnccnt tygargtncc nwsnccn                                         807
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<210> 4
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<213> Artificial Sequence

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<223> Pseudo repeat motif #1

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (19)...(20)
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<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (22)...(26)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (27)...(30)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (32)...(37)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (38)...(39)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (41)...(41)
<223> Xaa is any amino acid residue

<400> 4
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Cys Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
            20   25   30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35   40

<210> 5
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #2

<221> VARIANT
<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(15)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (16)...(17)
<223> Each Xaa is independently any amino acid residue
        or not present

<221> VARIANT
<222> (19)...(20)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (22)...(23)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(24)
<223> Each Xaa is independently any amino acid residue
        or not present

<221> VARIANT
<222> (26)...(33)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (34)...(36)
<223> Each Xaa is independently any amino acid residue
        or not present

<221> VARIANT
<222> (38)...(44)
<223> Each Xaa is independently any amino acid residue

<400> 5
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30

Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
            35   40   45

<210> 6
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<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (9)...(14)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (15)...(18)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT
<222> (31)...(38)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (39)...(39)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (41)...(47)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (49)...(49)
<223> Xaa is any amino acid residue or not present

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1   5   10   15
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
            20   25   30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
        35   40   45
Xaa

<210> 7
<211> 48
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<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #3 alternative motif

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<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

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<221> VARIANT
<222> (8)...(8)
<223> Xaa is independently any amino acid residue or not
      present

<221> VARIANT
<222> (10)...(13)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (14)...(18)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (31)...(40)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (41)...(46)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (48)...(48)
<223>  Xaa is any amino acid residue

<400> 7
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Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40                  45
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<210> 8
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #4

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (18)...(19)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (21)...(22)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(27)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (28)...(33)
<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT
<222> (35)...(37)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (38)...(41)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (43)...(43)
<223> Each Xaa is independently any amino acid residue

<400> 8
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Cys Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35   40

<210> 9
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #4 alternative motif

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<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(12)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (13)...(16)
<223> Each Xaa is independently any amino acid residue
      or not present

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<221> VARIANT
<222> (18)...(22)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (24)...(27)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (28)...(33)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (34)...(37)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (38)...(41)
<223> Each Xaa is independently any amino acid residue
      or not present

<221> VARIANT
<222> (43)...(43)
<223> Xaa is any amino acid residue
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Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40
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<211> 18
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<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25352
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<400> 10
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<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25353

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<210> 12
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<213> Artificial Sequence

<220>
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<211> 24
<212> DNA
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<220>
<223> oligonucleotide primer ZC25365

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<210> 14
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<223> oligonucleotide primer ZC25352

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    <210> 15
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Glu Tyr Met Pro Met Glu
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    <210> 17
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<220>
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<400> 18
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<211> 108
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<213> Homo sapiens

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<223> tPA leader

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<220>
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<210> 21
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<212> DNA
<213> Artficial sequence

<220>
<223> Polynucleotide Construct

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gagctatcca aggattgtgg ttatggagag ggtggagatg cctactgcac agcctgccct     240
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ccgtgcacga agcagacccc cacctctgag gttcaatgtg ccttccagtt gagcttagtg     480
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<210> 22
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<220>
<223> construct

<400> 22
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tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg     960
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aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1080
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
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        <210> 23
        <211> 47
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide ZC26463

        <400> 23
atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct   47

        <210> 24
        <211> 46
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide ZC26464

        <400> 24
taatacgact cactataggg aggggcccct gctgctgttg tggtat   46

        <210> 25
        <211> 49
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide ZC26470

        <400> 25
atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca   49

        <210> 26
        <211> 47
        <212> DNA
        <213> Artificial Sequence

<220>
<223> Oligonucleotide ZC26471

<400> 26
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat   47

<210> 27
<211> 297
<212> PRT
<213> Homo sapiens

<400> 27

```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1               5                  10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
            100                 105                 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
            115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
    130                 135                 140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145                 150                 155                 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
                165                 170                 175
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
            180                 185                 190
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
        195                 200                 205
Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser Ser
    210                 215                 220
```

Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
225   230   235   240
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
                245   250   255
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
                260   265   270
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
            275   280   285
Asn Val Pro Phe Glu Val Pro Ser Pro
    290   295

        <210> 28
        <211> 891
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> degenerate sequence

        <221> misc_feature
        <222> (1)...(891)
        <223> n = A,T,C or G

        <400> 28
atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn   60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay   120
tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn   180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay   240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar   300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty   360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn   420
gcnytngtnw snwsnytnyt ngtngtntty acnytngcnt tyytnggnyt nttyttyytn   480
taytgyaarc arttyttyaa ymgncaytgy carmgnggng gnytnytnca rttygargcn   540
gayaaracng cnaargarga rwsnytntty ccngtnccnc cnwsnaarga racnwsngcn   600
garwsncarg tnwsngaraa yathttycar acncarccny tnaayccnat hytngargay   660
gaytgywsnw snacnwsngg nttyccnacn cargarwsnt tyacnatggc nwsntgyacn   720
wsngarwsnc aywsncaytg ggtncaywsn ccnathgart gyacngaryt ngayytncar   780
aarttywsnw snwsngcnws ntayacnggn gcngaracny tnggnggnaa yacngtngar   840
wsnacnggng aymgnytnga rytnaaygtn ccnttygarg tnccnwsncc n   891

        <210> 29
        <211> 267
        <212> PRT

<213> Homo sapiens

<400> 29
```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1               5                   10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
                20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
            35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
                100                 105                 110
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
            115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Gly Gly
    130                 135                 140
Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
145                 150                 155                 160
Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
                165                 170                 175
Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
            180                 185                 190
Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
            195                 200                 205
Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
    210                 215                 220
Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
225                 230                 235                 240
Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
            245                 250                 255
Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
            260                 265
```

<210> 30
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence

<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

<400> 30
```
atggaytgyc argaraayga rtaytgggay cartgggggnm gntgygtnac ntgycarmgn      60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay     120
tgyacngcnt gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn     180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay     240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytncar     300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty     360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn     420
gcnytnggng gnytnytnca rttygargcn gayaaracng cnaargarga rwsnytntty     480
ccngtnccnc cnwsnaarga racnwsngcn garwsncarg tnwsngaraa yathttycar     540
acncarccny tnaayccnat hytngargay gaytgywsnw snacnwsngg nttyccnacn     600
cargarwsnt tyacnatggc nwsntgyacn wsngarwsnc aywsncaytg ggtncaywsn     660
ccnathgart gyacngaryt ngayytncar aarttywsnw snwsngcnws ntayacnggn     720
gcngaracny tnggnggnaa yacngtngar wsnacnggng aymgnytnga rytnaaygtn     780
ccnttygarg tnccnwsncc n                                              801
```

<210> 31
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(529)
<223> n = A,T,C or G

<400> 31
```
ggattcnatn nctgaggntg natggcnttc nagttnwgas tkagtggagg cagatgcasc      60
cacagtgccc gcctcaggag gycacacttg ttgcrmtggt gagcagcstg ctagtggtgt     120
ttrccctggc cttcctgggg ctcttcttcc tcwacygcaa gcagttcttc aacagacatt     180
gycagcsgng gaggtttgct gcagtttgag gctgatraaa cagcaaagga ggaatctstm     240
ttycycgtgc cacccagcaa ggagaccagt gctgagtccc aagtgagtga gaacatyttt     300
cakacccagm cacttaaccc tatcctyrag gacgactgca rctcgactag tggyttcccc     360
acacaggart mctttaccat ggcctyctgc acctyagaga gccactscca ctgggwccac     420
arccccatcg aatgcacaka gctggacctg caaaagtttt ccagctctgc ctcctatact     480
ggagctgara ccttggggggg aaacacagnc aaaagcactg ganacaggg               529
```

```
<210> 32
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 32
cagttgagct tagtggaggc agatgcaccc acagtgcccc ctcaggaggc cacacttgtt      60
gsactggagg tttgctgcag tttgaggctg ataaaacagc aaaggaggaa tctctcttns     120
ccgtgccacc cagcaaggag accagtgctg agtcccaagt gagtgagaac atctttcaga     180
cccagccact taaccctatc ctcgaggacg actgcagctc gactagtggc ttccccacac     240
aggagtcctt taccatggcc tcctgcacct cagagagcca ctcccactgg gtccacagcc     300
ccatcgaatg cacagagctg gacctgcaaa agttttccag ctctgcctcc tatactggag     360
ctgagacctt gggggggaaac acagtcgaaa gcactggaga c                        401
```

```
<210> 33
<211> 528
<212> DNA
<213> Homo sapiens

<400> 33
ctctgaggtt caatgtgcct tccagttgag cttagtggag gcagatgcac ccacagtgcc      60
ccctcaggag gccacacttg ttgcactggt gagcagcctg ctagtggtgt ttaccctggc     120
cttcctgggg ctcttcttcc tctactgcaa gcagttcttc aacagacatt gccagcgtgt     180
tgcaggaggt ttgctgcagt ttgaggctga taaaacagca aaggaggaat ctctcttccc     240
cgtgccaccc agcaaggaga ccagtgctga gtcccaagtg agtgagaaca tctttcagac     300
ccagccactt aaccctatcc tcgaggacga ctgcagctcg actagtggct tccccacaca     360
ggagtccttt accatggcct cctgcacctc agagagccac tcccactggg tccacagccc     420
catcgaatgc acagagctgg acctgcaaaa gttttccagc tctgcctcct atactggagc     480
tgagaccttg ggggaaaca cagtcgaaag cactggagac aggctgga                   528
```

```
<210> 34
<211> 175
<212> PRT
<213> Homo sapiens

<400> 34
```

```
Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala
1               5                   10                  15
Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser
            20                  25                  30
Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr
        35                  40                  45
Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly Leu
    50                  55                  60
Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro
65                  70                  75                  .80
Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn
                85                  90                  95
Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser
                100                 105                 110
Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys
        115                 120                 125
Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr
    130                 135                 140
Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala
145                 150                 155                 160
Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
                165                 170                 175
```

```
        <210> 35
        <211> 299
        <212> PRT
        <213> Homo sapiens

        <400> 35
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1               5                   10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
                85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
                100                 105                 110
```

```
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120             125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
        130                 135             140
Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145                 150             155                 160
Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly
            165             170             175
Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
            180             185             190
Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
        195             200             205
Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
    210             215             220
Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
225             230             235             240
Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
            245             250             255
Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
            260             265             270
Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
        275             280             285
Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
    290             295
```

```
<210> 36
<211> 431
<212> DNA
<213> Homo sapiens

<400> 36
ctc tga ggt tca atg tgc ctt cca gtt gag ctt agt gga ggc aga tgc    48
acc cac agt gcc ccc tca gga ggc cac act tgt tgc act gga ggt ttg    96
ctg cag ttt gag gct gat aaa aca gca aag gag gaa tct ctc ttc ccc   144
gtg cca ccc agc aag gag acc agt gct gag tcc caa gtg agt gag aac   192
atc ttt cag acc cag cca ctt aac cct atc ctc gag gac gac tgc agc   240
tcg act agt ggc ttc ccc aca cag gag tcc ttt acc atg gcc tcc tgc   288
acc tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca   336
gag ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct   384
gag acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg ga    431

<210> 37
<211> 142
```

<210> PRT
<213> Homo sapiens

<400> 37

```
Leu Gly Ser Met Cys Leu Pro Val Glu Leu Ser Gly Gly Arg Cys Thr
1               5                   10                  15
His Ser Ala Pro Ser Gly Gly His Thr Cys Cys Thr Gly Gly Leu Leu
            20                  25                  30
Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
        35                  40                  45
Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
    50                  55                  60
Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser Ser
65                  70                  75                  80
Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
            85                  90                  95
Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
            100                 105                 110
Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
        115                 120                 125
Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
    130                 135                 140
```

<210> 38
<211> 173
<212> PRT
<213> Homo sapiens

<400> 38

```
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1               5                   10                  15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
            20                  25                  30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
        35                  40                  45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
    50                  55                  60
Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65                  70                  75                  80
Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
            85                  90                  95
Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
            100                 105                 110
```

```
Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
        115                 120                 125
Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Glu Val
        130                 135                 140
Cys Cys Ser Leu Arg Leu Ile Lys Gln Gln Arg Arg Asn Leu Ser Ser
145                 150                 155                 160
Pro Cys His Pro Ala Arg Arg Pro Val Leu Ser Pro Lys
                165                 170
```

```
        <210> 39
        <211> 519
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> degenerate polynucleotide sequence

        <221> misc_feature
        <222> (1)...(519)
        <223> n = A,T,C or G

        <400> 39
atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn      60
tgyggnccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay     120
tgyacngct gyccnccnmg nmgntayaar wsnwsntggg gncaycayaa rtgycarwsn      180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay     240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnyincar     300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty     360
carytnwsny tngtngargc ngaygcnccn acngtnccnc cncargargc nacnytngtn     420
gcnytngarg tntgytgyws nytnmgnytn athaarcarc armgnmgnaa yytnwsnwsn     480
ccntgycayc cngcnmgnmg nccngtnytn wsnccnaar                            519
```

```
        <210> 40
        <211> 47
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> oligonucleotide ZC26463

        <400> 40
atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct                   47
```

<210> 41
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 26464

<400> 41
taatacgact cactataggg aggggcccct gctgctgttg tggtat   46

<210> 42
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC24670

<400> 42
atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca   49

<210> 43
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 26471

<400> 43
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat   47

<210> 44
<211> 657
<212> DNA
<213> murine

<400> 44
ggtggcatct ctcttccaat tggtctgatt gttggagtga catcactggg tctgctgatg   60
ttaggactgg tgaactgcat catcctggtg cagaggaaaa agaagccctc ctgcctacaa   120
agagatgcca aggtgcctca tgtgcctgat gagaaatccc aggatgcagt aggccttgag   180

```
cagcagcacc  tgttgaccac  agcacccagt  tccagcagca  gctccctaga  gagctcagcc      240
agcgctgggg  accgaagggc  gccccctggg  ggccatcccc  aagcaagagt  catggcggag      300
gcccaagggt  ttcaggaggc  ccgtgccagc  tccaggattt  cagattcttc  ccacggaagc      360
cacgggaccc  acgtcaacgt  cacctgcatc  gtgaacgtct  gtagcagctc  tgaccacagt      420
tctcagtgct  cttcccaagc  cagcgccaca  gtgggagacc  cagatgccaa  gccctcagcg      480
tccccaaagg  atgagcaggt  cccccttctct caggaggagt  gtccgtctca  gtccccgtgt      540
gagactacag  agacactgca  gagccatgag  aagcccttgc  cccttggtgt  gccggatatg      600
ggcatgaagc  ccagccaagc  tggctggttt  gatcagattg  cagtcaaagt  ggcctga         657
```

```
        <210> 45
        <211> 824
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> artificial cDNA sequence



        <400> 45
ggtaccgaat  tgtacgcgta  tggggacttc  ccatatcaat  cagggacttt  ccgctgggga       60
ctttccggtc  tgactcatgc  ttctgactca  tgcttggggtg acatcatctc  gactagtcgt      120
accttcccgt  aaatccctcc  ccttcccgga  attacacacg  cgtatttccc  agaaaaggaa      180
ctgtagattt  ctaggaattc  aatccttggc  cacgcgttta  caccggaagt  tttccatatt      240
aggaattcct  tccggtttcc  tttctcgagg  ccaccgtggt  tgagcccgac  actcattcat      300
aaaacgcttg  ttataaaagc  agtggctgcg  gcgccttcgt  actccaaccg  catctgcagc      360
gagcaactga  gaagccaagg  atccaggctg  aattcatggg  tctcaacccc  cagctagttg      420
tcatcctgct  cttcttctc   gaatgtacca  ggagccatat  ccacgyatgc  gacaaaaatc      480
acttgagaga  gatcatcggc  attttgaacg  aggtcacagg  agaagggacg  ccatgcacgg      540
agatggatgt  gccaaacgtc  ctcacagcaa  cgaagaacac  cacagagagt  gagctcgtct      600
gtagggcttc  caaggtgctt  cgcatatttt  atttaaaaca  tgggaaaact  ccatgcttga      660
agaagaactc  tagtgttctc  atggagctgc  agagactctt  tcgggctttt  cgatgcctgg      720
attcatcgat  aagctgcacc  atgaatgagt  ccaagtccac  atcactgaaa  gacttcctgg      780
aaagcctaaa  gagcatcatg  caaatggatt  actcgtagtc  taga                       824
```

```
        <210> 46
        <211> 47
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide sequence ZC28835
```

<400> 46
taatacgact cactataggg aggcccccaa ggtctcagct ccagtat   47

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide sequence ZC 28836

<400> 47
gcaccggtgg cctcctgagg gggcact   27

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC 28830

<400> 48
gcaccggtgg catctctctt ccaattggt   29

<210> 49
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC 28837

<400> 49
gctctagagg ggtcaggcca ctttgactg   29

<210> 50
<211> 1081
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA construct

<400> 50

```
atggattgcc aagaaaatga gtactgggac caatggggac ggtgtgtcac ctgccaacgg      60
tgtggtcctg gacaggagct atccaaggat tgtggttatg gagagggtgg agatgcctac     120
tgcacagcct gccctcctcg caggtacaaa agcagctggg gccaccacaa atgtcagagt     180
tgcatcacct gtgctgtcat caatcgtgtt cagaaggtca actgcacagc tacctctaat     240
gctgtctgtg gggactgttt gcccaggttc taccgaaaga cacgcattgg aggcctgcag     300
gaccaagagt gcatcccgtg cacgaagcag accccacct ctgaggttca atgtgccttc      360
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a                                                                    1081
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